

<110> Presnell, Scott R.  
Kindsvogel, Wayne

<130> 99-106

<151> 1999-12-23

<151> 2000-12-01

<160> 44

<170> FastSEQ for Windows Version 3.0

 $\langle 210 \rangle$  1

<211> 1116

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$ 

<221> CDS

<222> (21)...(557)

<400> 1

<400> 1  
 tcgagttaga attgtctgca atg gcc gcc ctg cag aaa tct gtg agc tct ttc 53  
 Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe  
 1 5 10

ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg 101  
Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu  
15 20 25

gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac 149  
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp  
30 35 40

aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg 197  
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu  
45 50 55

gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att 245  
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile  
60 65 70 75

ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg 293  
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu  
80 85 90

atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa 341  
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln  
95 100 105

tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc 389  
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala  
110 115 120

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437  
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu  
125 130 135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485  
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu  
140 145 150 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533  
Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe  
160 165 170

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac 587  
Met Ser Leu Arg Asn Ala Cys Ile  
175

taacccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca 647  
aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt 707  
tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag actttctaag 767  
catagatatt tattgataac atttcattgt aactggtgtt ctatacacag aaaacaattt 827  
attttttaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa 887  
aaaccctaa atagcttcat gtttccataa tcagtacttt atatttataa atgtatttat 947  
tattattata agactgcatt ttatttatat cattttatta atatggattt atttatagaa 1007

002221 52E4Z60

acatcattcg atattgctac ttgagtgtaa ggctaataatt gatatttatg acaataatta 1067  
tagagctata acatgtttat ttgacctcaa taaacacttg gatataccta 1116

<210> 2  
<211> 179  
<212> PRT  
<213> Homo sapiens

<400> 2

Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu  
1 5 10 15  
Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala  
20 25 30  
Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln  
35 40 45  
Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser  
50 55 60  
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe  
65 70 75 80  
His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu  
85 90 95  
Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln  
100 105 110  
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg  
115 120 125  
Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn  
130 135 140  
Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu  
145 150 155 160  
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn  
165 170 175  
Ala Cys Ile

<210> 3  
<211> 167  
<212> PRT  
<213> Homo sapiens

<400> 3

Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val  
1 5 10 15  
Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys  
20 25 30

002221"54E9460

Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala  
           35                          40                          45  
 Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly  
       50                          55                          60  
 Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met  
 65                          70                          75                          80  
 Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser  
                           85                          90                          95  
 Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg  
                           100                          105                          110  
 Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His  
                           115                          120                          125  
 Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly  
       130                          135                          140  
 Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met  
 145                          150                          155                          160  
 Ser Leu Arg Asn Ala Cys Ile  
                           165

<210> 4

<211> 501

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide of ZCYT018

<221> misc\_feature

<222> (1)...(501)

<223> n = A,T,C or G

<400> 4

atgggnacny tngcnacnws ntggytntytn ytnytngcny tnytngtnca rggnggngcn 60  
 gcngcncna thwsnwsnca ytgymgnytn gayaarwsna ayttycarca rccntayath 120  
 acnaaymgna cnttyatgyt ngcnaargar gcnwsnytn cngayaayaa yacngaygtn 180  
 mgnytnathg gngaraaryt nttycayggn gtnwsnatgw sngarmgntg ytayytnatg 240  
 aarcargtny tnaayttyac nytnngargar gtnytnttyc cncarwsnga ymgnttycar 300  
 ccntayatgc argargtngt nccnttyytn gcnmgnytnw snaaymgnyt nwsnacntgy 360  
 cayathgarg gngaygayyt ncayathcar mgnaaygtnc araarytnaa rgayacngtn 420  
 aaraarytng gngarwsngg ngarathaar gcathggng arytngayyt nytnttyatg 480  
 wsnytnmgna aygcntgyat h 501

00222T"5Z9460

23

<210> 9  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC13946

<400> 9  
 ccctgcagtg atcaacatgg ccaagttgac cagtgccggt 40

<210> 10  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC13945

<400> 10  
 gcccatggac tagtttcgaa aggtcgagtg tcagtcctgc tcctc 45

<210> 11  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC18698

<400> 11  
 tttttttctc gagacttttt tttttttttt tttt 34

<210> 12  
 <211> 18  
 <212> DNA  
 <213> Oligonucleotide primer Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC26414

<400> 12

002227-5-94250

agctgcctcc ttctcttg

18

<210> 13

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC26415

<400> 13

tagggctgct ggaagttg

18

<210> 14

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Glu-Glu (CEE) peptide Tag amino acid sequence

<400> 14

Glu Tyr Met Pro Met Glu

1

5

<210> 15

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> C-terminal FLAG peptide tag

<400> 15

Asp Tyr Lys Asp Asp Asp Asp Lys

1

5

<210> 16

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

002221 5264260

<223> Oligonucleotide primer ZC28590

<400> 16

ttgggtacct ctgcaatggc cgccctgcag aaatct 36

<210> 17

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28580

<400> 17

ttgggatcca atgcaggcat ttctcagaga cat 33

<210> 18

<211> 2831

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (34)...(1755)

<400> 18

tagaggccaa gggagggctc tgtgccagcc ccg atg agg acg ctg ctg acc atc 54  
Met Arg Thr Leu Leu Thr Ile  
1 5

ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat 102  
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp  
10 15 20

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg 150  
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu  
25 30 35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc 198  
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile  
40 45 50 55

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt 246

002221 522225 122220



Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp	Trp	Val	Ala	Lys	Lys	Gly	Cys	
				60					65					70		
cag	cgg	atc	acc	cgg	aag	tcc	tgc	aac	ctg	acg	gtg	gag	acg	ggc	aac	294
Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	Leu	Thr	Val	Glu	Thr	Gly	Asn	
			75					80					85			
ctc	acg	gag	ctc	tac	tat	gcc	agg	gtc	acc	gct	gtc	agt	gcg	gga	ggc	342
Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr	Ala	Val	Ser	Ala	Gly	Gly	
		90					95					100				
cgg	tca	gcc	acc	aag	atg	act	gac	agg	ttc	agc	tct	ctg	cag	cac	act	390
Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	
	105					110					115					
acc	ctc	aag	cca	cct	gat	gtg	acc	tgt	atc	tcc	aaa	gtg	aga	tcg	att	438
Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile	
120					125					130					135	
cag	atg	att	gtt	cat	cct	acc	ccc	acg	cca	atc	cgt	gca	ggc	gat	ggc	486
Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	Ile	Arg	Ala	Gly	Asp	Gly	
				140					145					150		
cac	cgg	cta	acc	ctg	gaa	gac	atc	ttc	cat	gac	ctg	ttc	tac	cac	tta	534
His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	Asp	Leu	Phe	Tyr	His	Leu	
			155				160						165			
gag	ctc	cag	gtc	aac	cgc	acc	tac	caa	atg	cac	ctt	gga	ggg	aag	cag	582
Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	Met	His	Leu	Gly	Gly	Lys	Gln	
		170					175					180				
aga	gaa	tat	gag	ttc	ttc	ggc	ctg	acc	cct	gac	aca	gag	ttc	ctt	ggc	630
Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	Pro	Asp	Thr	Glu	Phe	Leu	Gly	
	185					190					195					
acc	atc	atg	att	tgc	gtt	ccc	acc	tgg	gcc	aag	gag	agt	gcc	ccc	tac	678
Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	Ala	Lys	Glu	Ser	Ala	Pro	Tyr	
200					205					210					215	
atg	tgc	cga	gtg	aag	aca	ctg	cca	gac	cgg	aca	tgg	acc	tac	tcc	ttc	726
Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	Arg	Thr	Trp	Thr	Tyr	Ser	Phe	
				220					225					230		

002221 549460

tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc	774
Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys	
235 240 245	
tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc	822
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser	
250 255 260	
ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag	870
Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln	
265 270 275	
gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg	918
Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu	
280 285 290 295	
gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag	966
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu	
300 305 310	
ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta	1014
Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu	
315 320 325	
ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc	1062
Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro	
330 335 340	
cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc	1110
Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val	
345 350 355	
ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca	1158
Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro	
360 365 370 375	
ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc	1206
Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala	
380 385 390	
cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg	1254
Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met	
395 400 405	

09746375-122200

gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa 1302  
 Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys  
 410 415 420

cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc 1350  
 His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser  
 425 430 435

tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg 1398  
 Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met  
 440 445 450 455

gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc 1446  
 Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys  
 460 465 470

aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg 1494  
 Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly  
 475 480 485

aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag 1542  
 Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln  
 490 495 500

atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca 1590  
 Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro  
 505 510 515

tgt tcc ccc tcg gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc 1638  
 Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser  
 520 525 530 535

ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca 1686  
 Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser  
 540 545 550

gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc 1734  
 Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala  
 555 560 565

ctg act gtg cag tgg gag tcc tgaggggaat gggaaaggct tgggtgcttcc 1785

09746375-122200

Leu Thr Val Gln Trp Glu Ser  
570

tccctgtccc	taccagtg	cacatccttg	gctgtcaatc	ccatgcctgc	ccatgccaca	1845
cactctgcga	tctggcctca	gacgggtgcc	cttgagagaa	gcagagggag	tggcatgcag	1905
ggcccctgcc	atgggtgcgc	tcctcaccgg	aacaaagcag	catgataagg	actgcagcgg	1965
gggagctctg	gggagcagct	tgtgtagaca	agcgcgtgct	cgctgagccc	tgcaaggcag	2025
aaatgacagt	gcaaggagga	aatgcagga	aactcccag	gtccagagcc	ccacctccta	2085
acaccatgga	ttcaaagtgc	tcagggaatt	tgcctctcct	tgccccattc	ctggccagtt	2145
tcacaatcta	gctcgacaga	gcatgaggcc	cctgcctctt	ctgtcattgt	tcaaagggtg	2205
gaagagagcc	tggaaaagaa	ccaggcctgg	aaaagaacca	gaaggaggct	gggcagaacc	2265
agaacaacct	gcacttctgc	caaggccagg	gccagcagga	cggcaggact	ctagggaggg	2325
gtgtggcctg	cagctcattc	ccagccaggg	caactgcctg	acgttgacg	atttcagctt	2385
cattcctctg	atagaacaaa	gcgaaatgca	ggtccaccag	ggaggagagac	acacaagcct	2445
tttctgcagg	caggagtctc	agaccctatc	ctgagaatgg	ggtttgaaag	gaagggtgagg	2505
gctgtggccc	ctggacgggt	acaataacac	actgtactga	tgtcacaact	ttgcaagctc	2565
tgccttgggt	tcagcccata	tgggtcaaaa	ttccagcctc	accactcaca	agctgtgtga	2625
cttcaaacaa	atgaaatcag	tgcccagaac	ctcggtttcc	tcactctgtaa	tgtggggatc	2685
ataacaccta	cctcatggag	ttgtggtgaa	gatgaaatga	agtcatgtct	ttaaagtgtc	2745
taatagtgcc	tggtagatgg	gcagtgccca	ataaacggta	gctattttaa	aaaaaaaaaa	2805
aaaaaaaaaa	atagcgccg	cctcga				2831

<210> 19

<211> 574

<212> PRT

<213> Homo sapiens

<400> 19

Met	Arg	Thr	Leu	Leu	Thr	Ile	Leu	Thr	Val	Gly	Ser	Leu	Ala	Ala	His
1				5					10					15	
Ala	Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser
			20					25					30		
Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr
		35					40					45			
Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp
	50					55				60					
Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn
65					70				75					80	
Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val
				85				90					95		
Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg
			100					105					110		

002221-529460

Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys  
 115 120 125  
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr  
 130 135 140  
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe  
 145 150 155 160  
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln  
 165 170 175  
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr  
 180 185 190  
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp  
 195 200 205  
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp  
 210 215 220  
 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly  
 225 230 235 240  
 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys  
 245 250 255  
 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe  
 260 265 270  
 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp  
 275 280 285  
 Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile  
 290 295 300  
 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser  
 305 310 315 320  
 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln  
 325 330 335  
 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala  
 340 345 350  
 Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val  
 355 360 365  
 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys  
 370 375 380  
 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro  
 385 390 395 400  
 Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr  
 405 410 415  
 Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln  
 420 425 430  
 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln  
 435 440 445

Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu  
 450 455 460  
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val  
 465 470 475 480  
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu  
 485 490 495  
 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro  
 500 505 510  
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser  
 515 520 525  
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys  
 530 535 540  
 Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp  
 545 550 555 560  
 Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser  
 565 570

<210> 20  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC26665

<400> 20  
 cacacaggcc ggccaccatg gccgccctgc agaaatctg

39

<210> 21  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC26666

<400> 21  
 cacacaggcg cgcctcaaatt gcaggcattt ctcagag

37

<210> 22  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

002222T 54544250

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC14666

&lt;400&gt; 22

agccaccaag atgactga

18

&lt;210&gt; 23

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC14742

&lt;400&gt; 23

tgcatttggt aggtgcggtt ga

22

&lt;210&gt; 24

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC25963

&lt;400&gt; 24

agtcaacgca tgagtctctg aag

23

&lt;210&gt; 25

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC28354

&lt;400&gt; 25

accaacaaag agccattgac ttg

23

&lt;210&gt; 26

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

09746375-122200

<220>

<223> Oligonucleotide primer ZC21195

<400> 26

gaggagacca taacccccga cag

23

<210> 27

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC21196

<400> 27

catagctccc accacacgat ttt

23

<210> 28

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC14063

<400> 28

caccagacat aatagctgac agact

25

<210> 29

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC17574

<400> 29

ggtrttgctc agcatgcaca c

21

<210> 30

<211> 24

<212> DNA

00746375.122200



&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC17600

&lt;400&gt; 30

catgtaggcc atgaggtcca ccac

24

&lt;210&gt; 31

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC25964

&lt;400&gt; 31

gttcttgagt accccaacag tct

23

&lt;210&gt; 32

&lt;211&gt; 2149

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(693)

&lt;400&gt; 32

atg atg cct aaa cat tgc ttt cta ggc ttc ctc atc agt ttc ttc ctt  
 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
 1 5 10 15

48

act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag  
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln  
 20 25 30

96

agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag  
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
 35 40 45

144

cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac

192

09746375.122200

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr	
50 55 60	
aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt	240
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly	
65 70 75 80	
act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag	288
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln	
85 90 95	
gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca	336
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser	
100 105 110	
gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata	384
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile	
115 120 125	
gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta	432
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val	
130 135 140	
att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat	480
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn	
145 150 155 160	
gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att	528
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile	
165 170 175	
aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga	576
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg	
180 185 190	
gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg	624
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val	
195 200 205	
gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa	672
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu	
210 215 220	

00746375.122200

gag aga tgt gtg gaa att cca tgacttggtg aatttgcat tcagcaatgt 723  
 Glu Arg Cys Val Glu Ile Pro  
 225 230

ggaaattcta aagctccctg agaacaggat gactcgtgtt tgaaggatct tatttaaaat 783  
 tgtttttgta ttttcttaaa gcaatattca ctgttacacc ttggggactt ctttgtttat 843  
 ccattctttt atcctttata tttcatttta aactatattt gaacgacatt cccccgaaa 903  
 aattgaaatg taaagatgag gcagagaata aagtgttcta tgaaattcag aactttattt 963  
 ctgaatgtaa catcccta atacaacctt attcttctaa tacagcaaaa taaaaattta 1023  
 acaaccaagg aatagtattt aagaaaatgt tgaaataatt tttttaaaat agcattacag 1083  
 actgaggcgg tcctgaagca atgggttttt actctcttat tgagccaatt aaattgacat 1143  
 tgctttgaca atttaaaact tctataaagg tgaatatttt tcatacattt ctattttata 1203  
 tgaatatact ttttatatat ttattattat taaatatttc tacttaatga atcaaaattt 1263  
 tgtttttaaag tctactttat gttaaataaga acaggttttg gggaaaaaaa tcttatgatt 1323  
 tctggattga tatctgaatt aaaactatca acaacaagga agtctactct gtacaattgt 1383  
 ccctcattta aaagatatat taagcttttc ttttctgttt gtttttgttt tgtttagttt 1443  
 ttaatcctgt cttagaagaa cttatcttta ttctcaaaat taaatgtaat ttttttagtg 1503  
 acaagaaga aaggaaacct cattactcaa tccttctggc caagagtgtc ttgcttggtg 1563  
 cgcttcctc atctctatat aggaggatcc catgaatgat ggtttatttg gaactgctgg 1623  
 ggtcgacccc atacagagaa ctcagcttga agctggaagc acacagtggg tagcaggaga 1683  
 aggaccggtg ttggtagggt cctacagaga ctatagagct agacaaagcc ctccaaactg 1743  
 gccctcctg ctcactgcct ctcctgagta gaaatctggt gacctaaagg tcagtgcggt 1803  
 caacagaaag ctgccttctt cacttgaggc taagtcttca tatatgttta aggttgtctt 1863  
 tctagtgagg agatacatat cagagaacat ttgtacaatt ccccatgaaa attgctccaa 1923  
 agttgataac aatatagtcg gtgcttctag ttatatgcaa gtactcagt ataaatggat 1983  
 taaaaaatat tcagaaatgt attggggggg ggaggagaat aagaggcaga gcaagagcta 2043  
 gagaattggt ttccttgctt ccctgtatgc tcagaaaaca ttgatttgag catagacgca 2103  
 gagactgaaa aaaaaaaaaat gctcgagcgg ccgccatatc cttggt 2149

<210> 33

<211> 231

<212> PRT

<213> Homo sapiens

<400> 33

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
 1 5 10 15  
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln  
 20 25 30  
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
 35 40 45  
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
 50 55 60

09746375.122200

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
 65 70 75 80  
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
 85 90 95  
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
 100 105 110  
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
 115 120 125  
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
 130 135 140  
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
 145 150 155 160  
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
 165 170 175  
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
 180 185 190  
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
 195 200 205  
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
 210 215 220  
 Glu Arg Cys Val Glu Ile Pro  
 225 230

&lt;210&gt; 34

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human ZCYT018 peptide 1 (huZCYT018-1)

&lt;400&gt; 34

Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly  
 1 5 10 15  
 Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys  
 20 25

&lt;210&gt; 35

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

09746375.122200

<223> Human ZCYT018 peptide 2 (huZCYT018-2)

<400> 35

Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro Tyr Met Gln  
 1 5 10 15  
 Glu Val Val Pro Cys  
 20

<210> 36

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Human ZCYT018 peptide 3 (huZCYT018-3)

<400> 36

Cys Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser  
 1 5 10 15  
 Gly Glu Ile Lys Ala Ile Gly Glu  
 20

<210> 37

<211> 778

<212> DNA

<213> mus musculus

<220>

<221> CDS

<222> (47)...(583)

<400> 37

aggctctcct ctcaattatc aactgttgac acttgtgcga tcggtg atg gct gtc 55  
 Met Ala Val  
 1

ctg cag aaa tct atg agt ttt tcc ctt atg ggg act ttg gcc gcc agc 103  
 Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu Ala Ala Ser  
 5 10 15

tgc ctg ctt ctc att gcc ctg tgg gcc cag gag gca aat gcg ctg ccc 151  
 Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn Ala Leu Pro  
 20 25 30 35

00746376-122200

gtc aac acc cgg tgc aag ctt gag gtg tcc aac ttc cag cag ccg tac 199  
 Val Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln Gln Pro Tyr  
 40 45 50

atc gtc aac cgc acc ttt atg ctg gcc aag gag gcc agc ctt gca gat 247  
 Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu Ala Asp  
 55 60 65

aac aac aca gat gtc cgg ctc atc ggg gag aaa ctg ttc cga gga gtc 295  
 Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe Arg Gly Val  
 70 75 80

aat gct aag gat cag tgc tac ctg atg aag cag gtg ctc aac ttc acc 343  
 Asn Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu Asn Phe Thr  
 85 90 95

ctg gaa gac gtt ctg ctc ccc cag tca gac agg ttc cag ccc tac atg 391  
 Leu Glu Asp Val Leu Leu Pro Gln Ser Asp Arg Phe Gln Pro Tyr Met  
 100 105 110 115

cag gag gtg gtg cct ttc ctg acc aaa ctc agc aat cag ctc agc tcc 439  
 Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln Leu Ser Ser  
 120 125 130

tgt cac atc agc ggt gac gac cag aac atc cag aag aat gtc aga agg 487  
 Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn Val Arg Arg  
 135 140 145

ctg aag gag aca gtg aaa aag ctt gga gag agt gga gag atc aag gcg 535  
 Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile Lys Ala  
 150 155 160

att ggg gaa ctg gac ctg ctg ttt atg tct ctg aga aat gct tgc gtc 583  
 Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala Cys Val  
 165 170 175

tgagcgagaa gaagctagaa aacgaagaac tgctccttcc tgccttctaa aaagaacaat 643  
 aagatccctg aatggacttt tttactaaag gaaagtgaga agctaacgtc catcatcatt 703  
 agaagatttc acatgaaacc tggctcagtt gaaaaagaaa atagtgtcaa gttgtccatg 763  
 agaccagagg tagac 778

<211> 179  
 <212> PRT  
 <213> mus musculus

<400> 38

Met Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu  
 1 5 10 15  
 Ala Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn  
 20 25 30  
 Ala Leu Pro Val Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln  
 35 40 45  
 Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser  
 50 55 60  
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe  
 65 70 75 80  
 Arg Gly Val Asn Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu  
 85 90 95  
 Asn Phe Thr Leu Glu Asp Val Leu Leu Pro Gln Ser Asp Arg Phe Gln  
 100 105 110  
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln  
 115 120 125  
 Leu Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn  
 130 135 140  
 Val Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu  
 145 150 155 160  
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn  
 165 170 175  
 Ala Cys Val

<210> 39  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC37125

<400> 39  
 ctatttggcc ggccaccatg gctgtcctgc ag

<210> 40  
 <211> 32  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC37126

<400> 40

cgtagcgggcg cgcctcagac gcaagcattt ct

32

<210> 41

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28348

<400> 41

cgggatcccg atggccgccc tgcag

25

<210> 42

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28345

<400> 42

gctctagacc aatgcaggca tttctcag

28

<210> 43

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC447

<400> 43

taacaatttc acacagg

17

<210> 44

<211> 18

00222T 57E9H760



<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC976

<400> 44

cgttgtaaaa cgacggcc

002221 5789460